

SEQUENCE LISTING

I GENERAL INFORMATION:

(I) APPLICANT: Thomas, Lawrence J.

(II) TITLE OF INVENTION: PLASMID BASED VACCINE FOR
TREATING ATHEROSCLEROSIS

(III) NUMBER OF SEQUENCES: 10

(IV) CORRESPONDENCE ADDRESS:

A ADDRESSEE: Tarkwich & Associates
B STREET: 130 Bishop Allen Drive
C CITY: Cambridge
D STATE: Massachusetts
E COUNTRY: USA
F ZIP: 02139

(V) COMPUTER READABLE FORM:

A MEDIUM TYPE: Floppy disk
B COMPUTER: IBM PC compatible
C OPERATING SYSTEM: Windows 95/98
D SOFTWARE: Word 97

(VI) CURRENT APPLICATION DATA:

A APPLICATION NUMBER: (not yet assigned)
B FILING DATE: 30 April 2001
C CLASSIFICATION:

(VII) PRIOR APPLICATION DATA:

A APPLICATION: 08/640,713
B FILING DATE: 03 May 1995 (01.05.96)

(VIII) PRIOR APPLICATION DATA:

A APPLICATION: 08/800,967
B FILING DATE: 21 February 1997 (21.02.97)

(IX) PRIOR APPLICATION DATA:

A APPLICATION: 09/171,959
B FILING DATE: 29 October 1998 (29.10.98)

(X) ATTORNEY/AGENT INFORMATION:

A NAME: Leon R. Tarkwich
B REGISTRATION NUMBER: 30,237
C REFERENCE DOCKET NUMBER: TCS 414.2 US-1

(XI) INFORMATION FOR SEQ ID NO: 1:

(1) SEQUENCE CHARACTERISTICS:
A LENGTH: 1488 base pairs
B TYPE: nucleic acid
C STRANDEDNESS: single
D TOPOLOGY: linear
(2) MOLECULE TYPE: cDNA
(3) HYPOTHETICAL:
(4) ANTI SENSE:
(5) FEATURE: Structural coding sequence for

mature rabbit CETP

A: NAME:
B: LOCATION:
X PUBLICATION INFORMATION:
A AUTHORS: Nagashima, Mariko, et al.
B TITLE: Cloning and mRNA tissue
distribution of rabbit
cholesteryl ester transfer
protein
C JOURNAL: J. Lipid Res.
D VOLUME: 29
E ISSUE:
F PAGES: 1643 1649
G DATE: 1988
H RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

XI SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCTCCCAAAG GCGGCTCTCA CGAGGCTGGC ATCGTGTGTC GCATCACCAA	50
SCCGCCCTC TTGGTGTGTA ACCAAGAGAC GGGCAAGGTG GTCCAGACGG	100
CCTTCCAGCG CCGCGGTAT CCGGACGTC GGGGGAGAG GGGCGTGATG	150
CTCTCGGGC GGGTCAAGTA CCGGTGTC AACCTCCAGA TCAGGCCACT	200
CTCCATCGCC AGCAGCCAGG TGGAGCTGGT GSAAGCCAA ACCATCGACC	250
TGCCCATCCA GAAGTGTGCC GTGGTCTTCA AGGGGACCCCT GAACTACAGC	300
TACACGAGTG CCTGGGGCTT GGGCATCAAT CAGTCTGTGG ACTTCCAGAT	350
GAANTGTCCC ATTTACCTCC AGATCAACAC AGAGTTGACC TGGGAGGCTG	400
GCAGTGTCCC CACCAATGCC CCGGACTGCT ACCTGGGCTT CCATAAAGTG	450
CTCTGCACC TCCAGGGGGA GGGGAGGGG GGGTGGTCA AGCACTCTTT	500
CACAAACTTT ATCTCTTCA GGTBAAGGT GATTTBAAG CBAAGGTGT	550
GCAATCAGAT CAACACCATC TCCAAATCA TGGTBACTT TGTGAGAGC	600
AGGGCCGCCA GCATCTCTC ABATGGAGAC ATCGGGGGG ACATTTCCCT	650
GACGGGGGCC CCTGTATCA CAGCCACCTA CCGGAGTTC CATCACAAAG	700
ATCACTTAC GCACAGAAC GTCTCCGAGC CATTCCCTCT CCGGGCCCTC	750
CGGGGGGCTC TTCTGGGGGA CTCCCGCATC CTCTACTTCT GGTCTCCGA	800
TTAAATGCTC AACCTCTCTG CAGGGGGGCT CTTCCAGGAG GGGCGTCTG	850
TATTAATCTT CACAGGGCAT GATTTCAAGA AAGTCTCTGA GACCGAAT	900
TTAAATGCTC AACAGGAAT CTCTCAGGAG CTTTCCAGAG GCGTCCGAG	950
TTAAATGCTC CAATAGGCT TCCACTGCTT TAAGTGTCTT AAGATCTCTT	1000

JCCAGAAACCG GGSTGTGCGTG GTGTGTTCCTT CCCTCCGCGT GACGTTCCCG 1050
 TTCCCCCGCC CAGATGGCCC AGAAGCTGTG GCCTACAGGT TTGAGGAGGA 1100
 TATCATCACC ACCGTCGAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC 1150
 ACCCTCTTGA TTTCCAGTGC GTGCCCGCCA GCGGAAAGGC AGGCAGCTCA 1200
 JCAAATCTCT CCCTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCGAACCT 1250
 GACTGAGAGC CCCTCCGAGT CCCTGCAGAG CTCTCTGCGC TCCCTGATCG 1300
 CCACGGTGGG CATCCCGGAG GTCATGTCTC GGCTCGAGGT GGGCTTCACA 1350
 GCGCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA 1400
 GATTATCACT CTCGATGGCT GCTGTGCTGCT GCAGATGGAC TTCGGTTTTC 1450
 CCAAGCACCT GCTGCTGGAT TTCCTGCAGA GCTTGAGG 1486

2. INFORMATION FOR SEQ ID NO:2:

I. SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 amino acids
 (B) TYPE: amino acid
 D. TOPOLOGY: linear
 II. MOLECULE TYPE: protein
 III. HYPOTHETICAL:
 IV. ANTI SENSE:
 IX. FEATURE:
 A. NAME: Amino acid sequence for mature rabbit CETP protein.
 B. LOCATION:

X. PUBLICATION INFORMATION:
 A. AUTHORS: Nagashima, Mariko, et al.
 B. TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
 C. JOURNAL: J. Lipid Res.
 D. VOLUME: 29
 E. ISSUE:
 F. PAGES: 1643 - 1649
 G. DATE: 1988
 Y. RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

XI. SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Phe Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
 1 5 10
 Asp Ile Thr Lys Phe Ala Leu Leu Val Leu Asn Glu Glu
 15 20 25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
40 45 50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

His Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Tyr Phe Ser Asp Gln Val Leu Asn Ser Leu

265

270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430 435 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
460 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe
470 475 480

Ile Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
485 490

Leu Ser
495

2 INFORMATION FOR SEQ ID NO: 3:
 1 SEQUENCE CHARACTERISTICS:
 A LENGTH: 1428 base pairs
 B TYPE: nucleic acid
 3 STRANDEDNESS: single
 D TOPOLOGY: linear
 4 MOLECULE TYPE: cDNA
 5 HYPOTHETICAL:
 6 ANTI-SENSE:
 7 FEATURE
 A NAME: Structural coding sequence for
 mature human CETP
 B LOCATION:
 8 PUBLICATION INFORMATION:
 9A AUTHORS: Drayna, Dennis, et al.
 9B TITLE: Cloning and sequencing of
 human cholesteryl ester
 transfer cDNA
 C JOURNAL: Nature
 D VOLUME: 327
 E ISSUE:
 F PAGES: 632 - 634
 G DATE: 18-JUN-1987
 H RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

11 SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCTCCAAAG GCACCTGGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA	50
GGCTGCCCTC CTGGTGTGTA ACCACGAGAC TCCCAAGGTG ATCCAGACCG	100
CCTTCCAGCG AGCCAGCTAC CGAGATATCA CCGCCGAGAA GGCATGATG	150
CTCTTGGCC AAGTCAAGTA TGGGTTGCAC AACATCCAGA TCAGCCACTT	200
GTCCATCGCC ACCAGCCAGC TGGAGCTGGT GBAAGCCAG TCCATTGATG	250
TCTCCATTCA GAACCTGTCT CTGGTCTTCA ACGGAGCCCT GAAGTATGGC	300
TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT	350
TCACCTTCCC ATTGACCTCC AGATCAATAC ACAGCTGACC TGTGACTCTG	400
GTAGAGTGGG GACCGATGCC CCGACTGCT ACCTGTCTTT CCATAAGCTG	450
GGCTTCAATG TCCAACGGGA GCGAGACCCT GGSTGGATCA ACCAGTCTT	500
CACAAATTTG ATCTCCTTCA CCTTGAAGCT GGTCTTGAAG GACAGATCT	550
ATTAAGAGAT CAAGCTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA	600
AAGATTTTCA GCATCCCTTC AGATGGAGAC ATTGGGCTGG ACATTTCCCT	650
GAGATTTTAT GCGTCAATCA CAGCTCTCTA CCGGGAGTCC CATCAGAAAG	700
GTATTTTAT GTAGAAAT GTCTCAGAGG ACCTCCCTCT CCGATTTT	750

TGGCCACAC TSCCTGGGGGA GTCCCCCATG CTGTACTTCT GCTTCTCTGA 800
 GCGASTCTTC CACTCGCTGG CCAAGGTAGC TTTCAGGAT GGCCGCTCA 850
 TCTCAGCCT GATGGGAGAC GACTTCAAGG CACTGCTGA GACCTGGGGC 900
 TTCAACACCA ACCAGGAAAT CTTCAGAGG GTTGTGGGGC GCTTCCGCA 950
 CCAGGCCCAA GTACCGGTGC ACTGGCTCAA GATGDDCAAG ATCTCTGTC 1000
 AAAACAAGGG AGTCTGGGT AATTCCTCAG TGATGGTGAA ATTCTCTTT 1050
 CCACGCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT 1100
 CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC 1150
 TCITGGATTT CCAGATTACA CCAAAGACTG TTCCAACTT GACTGAGAGC 1200
 AGCTCCGAST CCATCCAGAG CTTCCTGAG TCAATGATCA CCGCTGTGG 1250
 CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTSTTTACA GCGCTCATGA 1300
 ACAGCAAAGG CGTGAAGCTC TTGACATCA TCAADCTGA GATTATCACT 1350
 CCAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT 1400
 CCTGCTGGAT TTCTCCAGA GCTTGGAGC 1428

1 INFORMATION FOR SEQ ID NO: 4:

1 SEQUENCE CHARACTERISTICS:

A LENGTH: 476 amino acids

B TYPE: amino acid

D TOPOLOGY: linear

I MOLECULE TYPE: peptide

II HYPOTHETICAL:

IV ANTI SENSE:

IX FEATURE:

(A) NAME: Amino acid sequence of mature human

CETP

B LOCATION:

X PUBLICATION INFORMATION:

A AUTHORS: Drayna, Dennis, et al.

B TITLE: Cloning and sequencing of human acyl-coenzyme A:cholesterol acyltransferase cDNA

C JOURNAL: Nature

D VOLUME: 327

E ISSUE:

F PAGES: 632-634

G DATE: 18 JUN 1987

H RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

X1 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15 20 25

Tyr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
30 35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180

Ile Tyr Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235 240 245

Phe Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
 250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
 265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
 275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
 290 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
 300 305 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
 315 320 325

Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
 330 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
 340 345 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
 355 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
 365 370 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
 380 385 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
 395 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
 405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
 420 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
 430 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
 445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
 460 465

Val Asp Phe Leu Gln Ser Leu Ser
 470 475

1 SEQUENCE CHARACTERISTICS:
A LENGTH: 169 base pairs
B TYPE: nucleic acid
C STRANDEDNESS: single
D TOPOLOGY: linear
ii MOLECULE TYPE:
iii HYPOTHETICAL:
iv ANTI-SENSE:
ix FEATURE:
A NAME:
B LOCATION:

xi SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CCGCCCCCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC      50
CGAGCGCTTC CCGCGCCAG ATGGCGAGA AGCTGTGGCC TACAGGTTTG      100
ACCACGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGGG TTTCCTGCAG      150
AGCCTGAGCT AGCGGCGGC                                         169
```

2 INFORMATION FOR SEQ ID NO: 6:

1 SEQUENCE CHARACTERISTICS:
A LENGTH: 169 base pairs
B TYPE: nucleic acid
C STRANDEDNESS: single
D TOPOLOGY: linear
ii MOLECULE TYPE: DNA
iii HYPOTHETICAL:
iv ANTI-SENSE:
ix FEATURE:
A NAME: Complementary strand to SEQ ID NO:5
B LOCATION: 1 to 169

xi SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
CCGCCCCCTA GGTACAGCTC TGCAGGAAAT CCACAGCCAG CTCCTTCCCA      50
AAACCGAAGA TATCTCTCTC AAACCTGTAG GGCACAGCTT CTGGCCCATC      100
TTCGCGGCGG AAGCGCTCCG TGATCCCGAT GAACTTGGAG TTGGCCTTGA      150
TGTACTGCAT CCGCGCGGC                                         169
```

3 INFORMATION FOR SEQ ID NO:7:

1 SEQUENCE CHARACTERISTICS:
A LENGTH: 50 amino acids
B TYPE: amino acid
D TOPOLOGY: linear
ii MOLECULE TYPE: peptide
iii HYPOTHETICAL:
iv ANTI-SENSE:
ix FEATURE: amino acid sequence of peptide encoded
by bases 11 to 169 of SEQ ID NO:5

A NAME:
B LOCATION:

xj. SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1 5 10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
15 20 25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40 45 50

2. INFORMATION FOR SEQ ID NO:8:

1. SEQUENCE CHARACTERISTICS:

A LENGTH: 1608 base pairs

B TYPE nucleic acid

C STRANDEDNESS: Single

D TOPOLOGY: linear

II. MOLECULE TYPE:

III. HYPOTHETICAL:

IV. ANTI SENSE:

V. FEATURE:

A NAME translational stop codon

B LOCATION: 1606 1608

xj. SEQUENCE DESCRIPTION: SEQ ID NO:8:

JJCCCTCAGT ATGTTGTTGA TTCTTCTAAA TCTTTTGTTG TGGAAAAGTT 50
TTCTTCTTAC CACGGGACTA AACCTGGTTA TGTAGATTCC ATTCAAAAAG 100
GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATGA CCATGATTGG 150
AAAGGGTTTT ATAGTACCGA CAATAAATAC CACGGCTCCGG GATACTCTGT 200
ABATAATGAA ACCCCCTCT CTGAAAAAGC TGGAGCCCTG GTCAAACTGA 250
GATATCCAGG ACTGACCAAG GTTCTCGCAC TAAAAGTGGT TATGCCGAA 300
ACTATTAAGA AAGAJTTAGG TTAAAGTCTC ACTGAACTGT TATCCAGCA 350
ANTGCGAAGG GAAGAGTTTA TCAAAAAGTT CGGTGATGGT CCTTCGCCCTG 400
TASTGCTCAG CCTTCCTTTC CCTGAGGGGA GTTCTAGGGT TGAATATATT 450
GATAATGAGG AACAGCCGAA ACCCTTAAGC GTAGAACTTG AGATTATTT 500
TAAAATATG GAAAAAGCTG GCAAGATTCG GATGTATGAG TATATGCTC 550
AAATTTATG AAAAAATCTT TCCAGCCGAT GASTAGCTAG CTGATTCTTA 600

TGCATAAATC TTGATTGGGA TGTCATAAGG CATAAAAACTA AGACAAAGAT 650
 AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700
 CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATAAOT ACAAGCAATTY 750
 CATCAAAACGG CATTAGAGCA TCCYGAATTG TCAGAACTTA AAACCGTTAC 800
 TGGBACCAAT CCTGTATTTCG CIGGGGGCTAA CTATCGGGCG TGGBCASTAA 850
 ACCTTCCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900
 ACTGCTGCTC TTTGATACT TCCYGTATC GGTAGOOTAA TGGBCATTGC 950
 AGACCGTGGC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000
 CTTTATCGTC TTTAATGGTT GCTDAAGCTA TCCATTGGT AGGAGAGCTA 1050
 JTTCATATTG GTTTGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100
 ATTTCAAGTA GTTCATAATT GSTATAATCG TCCCGGCTAT TCTCCGGGGC 1150
 ATAAAACGCA ACCATTTCTT CATBADGGT ATGCTGTGAG TTGAAACAGT 1200
 GTTGAAGATT CGATAATCCG AACIGTTTTT CAAGGGGAGA GTGGGCACGA 1250
 CATAAAAATT ACTGCTGAAA ATATCTTGT TCGAATGGC GGTGTCTAC 1300
 TACCGACTAT TCCYGGAAAG CTGSAAGTTA ATAAJTCGA GACTCATATT 1350
 TCGTAAATG GTCGGAAAAT AAGSAGGGT TCGAJAGCTA TAGACGGTGA 1400
 TSTAACTTTT TGTGCGCTTA AATCTCGGT TTATGTITGT AATGGTGTGC 1450
 ATCGAATCT TCACGTGGCA TTTCADAGAA GCAGCTCGGA GAAAAATCAT 1500
 TCTAATGAAA TTTGCTCGSA TTCCATAGGC GTTCTTGGT ACCAGAAAAC 1550
 AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGGTATTT TTTGAAATCA 1600
 AAAGCTGA 1608

2 INFORMATION FOR SEQ ID NO:9:

1 SEQUENCE CHARACTERISTICS:

A LENGTH: 535 amino acids

B TYPE: amino acid

C TOPOLOGY: linear

D MOLECULE TYPE: protein

E HYPOTHETICAL:

F ANTI-SENSE:

G FEATURE: A NAME:
B LOCATION:

3 SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 5 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
30 35 40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
60 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
130 135 140

Ala Gln Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155 160 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
170 175 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
185 190 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
200 205 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
215 220

Phe Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225 230 235

Phe Gln Gln Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
240 245 250

Thr Ala Leu Gln His Pro Gln Leu Ser Glu Leu Lys Thr Val
255 260 265

Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
 270 275 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
 285 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
 295 300 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
 310 315 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
 325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
 340 345 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
 355 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
 365 370 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
 380 385 390

Gly Tyr Ala Val Ser Tip Asn Thr Val Glu Asp Ser Ile Ile
 395 400 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
 410 415 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
 425 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
 435 440 445

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
 450 455 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
 465 470 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
 480 485 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
 495 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
 505 510 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
 520 525 530

100 100 100
538

1 INFORMATION FOR SEQ ID NO:10
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 21 amino acids
4 TYPE: amino acid
5 TOPOLOGY: linear
6 MOLECULE TYPE: protein
7 HYDROPHILIC:
8 ANTI-SENSE:
9 FEATURE:
A NAME:
B LOCATION:

10 SEQUENCE DESCRIPTION: SEQ ID NO: 10:

100 100 100
1 Ile Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
2 5 10

100 100 100
1 Lys Val Ser Ala Ser His Leu Glu
2 15 20